

Title: ISOLATED HUMAN KINASE PROTEINS...

1 CAGCACGAGG AACTCCTTCT GATCACCTGG CCAGCTGAGG TCAGAGTGGG
 51 AGAGGCAGTG GTTCCATTGA AGGAGTACTC CTAACGTGCA GAAGCCTGGG
 101 CGGTACAGAT GGGGTGCTGT CGCTTGGGCT GCGGGGGGTG TTCAGTTGCC
 151 CACAGTGTAT CTCAGGTCTT CACCAACCAT CCAAGCATGG TAGGCTGTGG
 201 CTGGCACCCA GGGTTGTGTG GCTGGGGAGG TGGTCTCCAC AGTTCCCTCC
 251 CTGCCCTCCC AGGGCCCCCA TCCATGCAGG TAACCATCGA GGATGTGCAG
 301 GCACAGACAG GCGGAACGGC CCAATTGAGG GCTATCATTG AGGGCGACCC
 351 ACAGCCCTCG GTGACCTGGT ACAAGGACAG CGTCCAGCTG GTGGACAGCA
 401 CCCGGCTTAG CCAGCAGCAA GAAGGCACCA CATACTCCCT GGTGCTGAGG
 451 CATGTGGCCT CGAAGGATGC CGGCGTTTAC ACCTGCCTGG CCCAAAACAC
 501 TGGTGGCCAG GTGCTCTGCA AGGCAGAGCT GCTGGTGCTT GGGGGGGACA
 551 ATGAGCCGGA CTCAGAGAAG CAAAGCCACC GGAGGAAGCT GCACTCCTTC
 601 TATGAGGTCA AGGAGGAGAT TGGAAGGGGC GTGTTTGGCT TCGTAAAAAG
 651 AGTGCAGCAC AAAGGAAACA AGATCTGTGT CGCTGCCAAG TTCATCCCCC
 701 TACGGAGCAG AACTCGGGCC CAGGCATACA GGGAGCGAGA CATCCTGGCC
 751 CGGCTGAGCT ACCCGCTGGT CACGGGGCTG CTGGACCACT TTGAGACCCG
 801 CAAGACCTTC ATCCTCATCC TGGAGCTGTG CTCATCCGAG GAGCTGCTGG
 851 ACCGCCTGTA CAGGAAGGGC GTGGTGACGG AGGCCGAGGT CAAGGTCTAC
 901 ATCCAGCAGC TGGTGGAGGG GCTGCACTAC CTGCACAGCC ATGGCGTTCT
 951 CCACCTGGAT ATAAAGCCCT CTAACATCCT GATGTTGCAT CCTGCCCGGG
 1001 AAGACATTAA AATCTGCGAC TTTGGCTTTG CCCAGAACAT CACCCCAGCA
 1051 GAGCTGCAGT TCAGCCAGTA CGGCTCCCTT GAGTTTCTCT CCCCCGAGAT
 1101 CATCCAGCAG AACCTGTGTA GCGAAGCCTC CGACATTTGG GCCATGGGTG
 1151 TCATCTCCTA TCCAGCCTG ACCTGCTCAT CCCCATTTGC CGGCGAGAGT
 1201 GACCGTGCCA CCTCTCTGAA CGTCTCTGGG GGGCGCGTGT CATGGAGCAG
 1251 CCCCATGCTG GCCCACCTCA GCGAAGACGC CAAAGACTTC ATCAAGGCTA
 1301 CGCTGCAGAG AGCCCCCTAG GCCCGGCCA GTGCGGCCCA GTGCCTCTCC
 1351 CACCCCTGGT TGCCGAAATC CATGCCCTGC GAGGAGGCCC ACTTCATCAA
 1401 CACCAAGCAG CTCAGTTTCC TCCTGGCCCG AAGTCGCTGG CAGCGTTCCC
 1451 TGATGAGCTA CAAGTCCATC CTGGTGATGC GCTCCATCCC TGAGCTGTGT
 1501 CGGGGCCAC CCGACAGCCC CTCCTCGGC GTAGCCCGGC ACCTCTGCAG
 1551 GGACACTGGT GCCTCCTCCA GTTCTCTCTC CTCCTCTGAC AACGAGCTGT
 1601 CCCCATTTGC CCGGGCTAAG TCACTGCCAC CCTCCCCGGT GACACACTCA
 1651 CCACTGTGTC ACCCCCGGGG CTTCTCTGCG CCCTCGGCCA GCCTGCCTGA
 1701 GGAAGCCGAG GCCAGTGAGC GCTCCACCGA GGCCCCAGCT CCGCCTGCAT
 1751 CTCCTGAGGG TGCCCGGCCA CCGGCGGCCC AGGGCTGCGT GCCCGGCAC
 1801 AGCGTCATCC GCAGCCTGTT CTACCACCAG GCGGGTGAGA GCCCTGAGCA
 1851 CGGGGCCCTG GCCCGGGGA GCAGGCGGCA CCCGGCCCGG CGGCGGCACC
 1901 TGCTGAAGGG CGGCTACATT GCGGGGGCGC TGCCAGGCCT GCGCGAGCCA
 1951 CTGATGGAGT GCGCGTGCT GGAGGAGGAG GCCGCCAGGG AGGAGCAGCG
 2001 CACCCCTCTG GCCAAAGCCC CCTCATTCGA GACTGCCCTC CGGCTGCCTG
 2051 CCTCTGGCAC CCACTTGGCC CCTGGCCACA GCCACTCCCT GGAACATGAC
 2101 TCTCCGAGCA CCCCCCGCCC CTCCTCGGAG GCCTGCGGTG AGGCACAGCG
 2151 ACTCCCTTCA GCCCCCTCCG GGGGGGGCCC TATCAGGGAC ATGGGGCACC
 2201 CTCAGGGCTC CAAGCAGCTT CCATCCACTG GTGGCCACCC AGGCACTGCT
 2251 CAGCCAGAGA GGCCATCCCC GGACAGCCCT TGGGGGCAGC CAGCCCTTTT
 2301 CTGCCACCCC AAGCAGGGTT CTGCCCCCA GGAGGGCTGC AGCCCCCACC
 2351 CAGCAGTTGC CCCATGCCCT CTGGCTCCT TCCCTCCAGG ATCTTGCAAA
 2401 GAGGCCCTCT TAGTACCCTC AAGCCCCCTT TTGGGACAGC CCCAGGCACC
 2451 CCCTGCCCTT GCCAAAGCAA GCCCCCATT GGAATCTAAG ATGGGGCCTG
 2501 GAGACATCTC TCTTCTGGG AGGCCAAAAC CCGGCCCTGT CAGTTCCCCA
 2551 GGGTCAGCCT CCCAGGCGAG CTCTTCCCAA GTGAGCTCCC TCAGGTGGG
 2601 CTCTCTCCAG GTGGGCACAG AGCCTGGCCC CTCCTGGAT GCGGAGGGCT
 2651 GGACCCAGGA GGCTGAGGAT CTGTCCGACT CCACACCCAC CTTGCAGCGG
 2701 CCTCAGGAAC AGGTGACCAT GCGCAAGTTC TCCCTGGGTG GTCGCGGGG
 2751 CTACGCAGGC GTGGCTGGCT ATGGCACCTT TGCCCTTGGT GGAGATGCAG
 2801 GGGGCATGCT GGGGCAGGGG CCCATGTGGG CCAGGATAGC CTGGGCTGTG
 2851 TCCAGTCCG AGGAGGAGGA GCAGGAGGAG GCCAGGCTG AGTCCAGTC
 2901 GGAGGAGCAG CAGGAGGCCA GGGCTGAGC CCCACTGCCC CAGGTCACTG
 2951 CAAGGCCTGT CCGTAGGTC GGCAGGGCTC CCACCAGGAG CTCTCCAGAG
 3001 CCCACCCCAT GGGAGGACAT CGGGCAGGTC TCCCTGGTGC AGATCCGGGA
 3051 CCTGTCAAGT GATGCGGAGG CGGCCGACAC AATATCCCTG GACATTTCCG
 3101 AGGTGGACCC CGCCTACCTC AACCTCTCAG ACCTGTACGA TATCAAGTAC
 3151 CTCCTCTTGC AGTTTATGAT CTTCAGGAAA GTCCCCAAGT CCGCTCAGCC
 3201 AGAGCCGCCC TCCCCATGG CTGAGGAGGA GCTGGCCGAG TTCCCGGAGC
 3251 CCACGTGGCC CTGGCCAGGT GAACTGGGCC CCCACGCAGG CCTGGAGATC
 3301 ACAGAGGAGT CAGAGGATGT GGACGCGCTG CTGGCAGAGG CTGCGCTGGG
 3351 CAGGAAGCGC AAGTGGTCCT CGCCGTACAG CAGCCTCTTC CACTTCCCTG
 3401 GGAGGCACCT GCCGCTGGAT GAGCCTGCAG AGCTGGGGCT GCGTGAGAGA
 3451 GTGAAGGCCT CCGTGAGACA CATCTCCCGG ATCCTGAAGG GCAGGCCGGA

FIGURE 1A

Docket No.: CL000927-CIP-DIV2

Serial No.: To be assigned

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3501 AGGTCTGGAG AAGGAGGGGC CCCCAGGAA GAAGCCAGGC CTGCTTCTCT
3551 TCCGGCTCTC AGGTCTGAAG AGCTGGGACC GAGCGCCGAC ATTCCTAAGG
3601 GAGCTCTCAG ATGAGACTGT GGTCTGGGC CAGTCAGTGA CACTGGCCTG
3651 CCAGGTGTCA GCCCAGCCAG CTGCCCAGGC CACCTGGAGC AAAGACGGAG
3701 CCCCCCTGGA GAGCAGCAGC CGTGTCTCTA TCTCTGCCAC CCTCAAGAAC
3751 TTCCAGCTTC TGACCATCCT GGTGGTGGTG GCTGAGGACC TGGGTGTGTA
3801 CACCTGCAGC GTGAGCAATG CGCTGGGGAC AGTGACCACC ACGGGCGTCC
3851 TCCGGAAGGC AGAGCGCCCC TCATCTTCGC CATGCCCGGA TATCGGGGAG
3901 GTGTACGCGG ATGGGGTGCT GCTGGTCTGG AAGCCCGTGG AATCCTACGG
3951 CCCTGTGACC TACATTGTGC AGTGCAGCCT AGAAGGCGGC AGCTGGACCA
4001 CACTGGCCTC CGACATCTTT GACTGCTGCT ACCTGACCAG CAAGCTCTCC
4051 CGGGGTGGCA CCTACACCTT CCGCACGGCA TGTGTAGCA AGGCAGGAAT
4101 GGTGTCCTAC ACAGACCCCT CGGAGCAAGT CCTCTGGGA GGGCCCAGCC
4151 ACCTGGCCTC TGAGGAGGAG AGCCAGGGGC GGTGAGCCCA ACCCCTGCCC
4201 AGCACAAAGA CCTTCGCATT CCAGACACAG ATCCAGAGGG GCGCTTCAG
4251 CGTGGTGCGG CAATGCTGGG AGAAGGCCAG CGGGCGGGCG CTGGCCGCCA
4301 AGATCATCCC CTACCACCCC AAGGACAAGA CAGCAGTGCT GCGCAATAC
4351 GAGGCCCTCA AGGGCCTGCG CCACCCGCAC CTGGCCAGC TGCACGAGC
4401 CTACCTCAGC CCCCAGCACC TGGTGTCTAT CTTGGAGCTG TGCTCTGGGC
4451 CCGAGCTGCT CCCCTGCCTG GCCGAGAGGG CCTCTACTC AGAATCTGAG
4501 GTGAAGGACT ACCTGTGGCA GATGTGAGT GCCACCCAGT ACCTGCACAA
4551 CCAGCACATC CTGCACCTGG ACCTGAGGTC CGAGAACATG ATCATCACCG
4601 AATACAACTT GCTCAAGGTC GTGGACCTGG GCAATGCACA GAGCCTCAGC
4651 CAGGAGAAGG TGCTGCCCTC AGACAAGTTC AAGGACTACC TAGAGACCAT
4701 GGTCTCCAGG TCCTTGGAGG GCCAGGGGGC TGTTCACAG ACAGACATCT
4751 GGGCCATCGG TGTGACAGCC TTCATCATGC TGAGCGCCGA GTACCCGGTG
4801 AGCAGCGAGG GTGCACGCGA CCTGCAGAGA GGAATGCGCA AGGGGCTGGT
4851 CCGGCTGAGC CGCTGTCTAC CGGGGCTGTC CGGGGGCGCC GTGGCCTTCC
4901 TGGCAGCAGC TCTGTGCGCC CAGCCCTGGG GCCGGCCCTG CGCGTCCAGC
4951 TGCCTGCAGT GCCCGTGGCT AACAGAGGAG GGCCCGGCCT GTTCGCGGCC
5001 CGCGCCCCGTG ACCTTCCCTA CCGCGCGGCT GCGCGTCTTC GTGCGCAATC
5051 GCGAGAAGAG ACGCGCGCTG CTGTACAAGA GGCACAACCT GGCCAGGTG
5101 CGCTGAGGGT CGCCCCGGCC ACACCCTTGG TCTCCCGCT GGGGGTCTGCT
5151 GCAGACGCGC CAATAAAAC GCACAGCCGG GCGAGAAAAA AAAAAAAAAA
5201 AAAAAAA (SEQ ID NO:1)
```

FEATURES:

Start: 109

Stop: 5104

Homologous proteins:

Top BLAST Hits:

	Score	E
gi 7242949 dbj BAA92535.1 (AB037718) KIAA1297 protein [Homo sa...	425	e-117
gi 8928460 sp O75962 TRIO_HUMAN TRIPLE FUNCTIONAL DOMAIN PROTEI...	229	1e-58
gi 6005922 ref NP_009049.1 triple functional domain (PTPRF int...	229	1e-58
gi 3024081 sp Q15746 KMLS_HUMAN MYOSIN LIGHT CHAIN KINASE, SMOO...	206	2e-51
gi 90103 pir A41674 myosin-light-chain kinase (EC 2.7.1.117), ...	205	4e-51
gi 7239696 gb AAC18423.2 (U48959) myosin light chain kinase [H...	204	6e-51
gi 7239698 gb AAD15921.2 (AF069601) myosin light chain kinase ...	204	6e-51
gi 1103677 emb CAA62378.1 (X90870) myosin-light-chain kinase [...	204	6e-51
gi 3024085 sp Q28824 KMLS_BOVIN MYOSIN LIGHT CHAIN KINASE, SMOO...	203	1e-50
gi 2851405 sp P29294 KMLS_RABIT MYOSIN LIGHT CHAIN KINASE, SMOO...	203	1e-50
gi 3982821 gb AAC83683.1 (AF081663) myosin light chain kinase ...	198	3e-49
gi 3982823 gb AAC83684.1 (AF081664) myosin light chain kinase ...	198	3e-49
gi 3982827 gb AAC83686.1 (AF081666) myosin light chain kinase ...	198	3e-49
gi 3982807 gb AAC83676.1 (AF081656) myosin light chain kinase ...	198	3e-49

BLAST dbEST hit:

gi|7958129 /dataset=dbest /taxon=960...

1283 0.0

EXPRESSION INFORMATION FOR MODULATORY USE:

From BLAST dbEST hit:

gi|7958129 Human Colon carcinoma

From PCR-based tissue screening panels:

Human Placenta

Human Kidney

Human Lung

Human skeletal muscle

Human heart

Human fetal whole brain

FIGURE 1B

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1  MGCCRLGCGG  CSAHVSQ  LTNHPSMVGC  GWHPLCGWG  GGLHSSLPAL
51  PGPPSMQVTI  EDVQAQTGGT  AQFEAIIEGD  PQPSVTWYKD  SVQLVDSTRL
101  SQQEGTITYS  LVLRHVASKD  AGVYTCLAQN  TGGQVLCKAE  LLVLGGDNEP
151  DSEKQSHRRK  LHSFYEVKEE  IGRGVFGFVK  RVQHKGNKIL  CAAKFIPLRS
201  RTRAQAYRER  DILAALSHPL  VTGLLDQFET  RKTLLILEL  CSSEELDLRL
251  YRKGVTTEAE  VKVYIQQLVE  GLHYLHSHGV  LHLDIKPSNI  LMVHPAREDI
301  KICDFGFAQN  ITPAELQFSQ  YGSPFVSPE  IIQNPVSEA  SDIWMGVIS
351  YLSLTCSPPF  AGESDRATLL  NVLEGRVSW  SPMAAHLSED  AKDFIKATLQ
401  RAPQARPSAA  QCLSHPWFLK  SMPAEAHFI  NTKQLKFLA  RSRWQSLMS
451  YKSILVMRSI  PELLRGPPDS  PSLGVARHLC  RDTGSSSSSS  SSSDNELAPF
501  ARAKSLPPSP  VTHSPLLHPR  GFLRPSASLP  EEAEASERST  EAPAPPASPE
551  GAGPPAQC  VPRHSVIRSL  FYHQAGESPE  HGALAPGSR  HPARRRHLLK
601  GGYIAGALPG  LREPLMEHRV  LEEEAAREEQ  ATLLAKAPSF  ETALRLPASG
651  THLAPGSHS  LEHDSPTPR  PSSEACGEAQ  RLPSAPSGGA  PIRDMGHPQG
701  SKQLPVTGGH  PGTAQPERPS  PDSWPQGPAP  FCHPKQGSAP  QEGCSPHAPV
751  APCPPGSFPF  GSCKEAPLVP  SSPFLGQPQA  PPAPAKASPP  LDSKMGPGDI
801  SLPGRPKPGP  CSSPGSASQA  SSSQVSSLRV  GSSQVGTEPG  PSLDAEGWTQ
851  EAEDLSDSTP  TLQRPQEQVT  MRKFSLGGRG  GYAGVAGYGT  FAFGGDAGGM
901  LGQGPWMARI  AWAVSQSEEE  EQEAREAESQ  SEEQEARAE  SPLPQVSARP
951  VPEVGRAPTR  SSPETPWED  IGQVSLVQIR  DLSGDAEAD  TISLDISEVD
1001  PAYLNLSDLY  DIKYLPEFEM  IFRKVPKSAQ  PEPPSPMAEE  ELAEFPEPTW
1051  PWGELGPHA  GLEITEESD  VDALLAEAAV  GRKRKWSPP  RSLFHFPGRH
1101  LPLDEPABLG  LRERVKASVE  HISRLKGRP  EGLEKEGPP  KKPGLASFRL
1151  SGLKSWDRAP  TFLRELSDET  VVLGQSVTLA  CQVSAQPAAQ  ATWSKDGAPL
1201  ESSSRVLISA  TLKNFQLTI  LVVVAEDLGV  YTCVSNALG  TVTTTGVLRK
1251  AERPSSPCP  DIGEVYADGV  LLVWKPVESY  GPVTYIVQCS  LEGGSWTTLA
1301  SDIFDCCYLT  SKLSRGTYT  FRTACVSKAG  MGPYSSPSEQ  VLLGGPSHLA
1351  SEESQGRSA  QPLPSTKTFA  FQTQIQGRF  SVVRQCWEKA  SGRALAAKII
1401  PYHPKDKTAV  LREYEALKGL  RHPHLAQLHA  AYLSPRHLVL  ILELCSPGEL
1451  LPCLAERASY  SESEVKDYLV  QMSATQYLH  NQHILHLDLR  SENMIITEYN
1501  LLKVVDLUNA  QSLSQEKVLP  SDKFKDYLET  MAPELLEGQG  AVPQTDIWI
1551  GVTAFIMLSA  EYPVSSEGAR  DLQRLKRLGL  VRLSRCYAGL  SGGAVAFRLS
1601  TLCAQPWGRP  CASSCLQCPW  LTEEGPACSR  PAPVTFPTAR  LRVFVRNREK
1651  RRALLYKRHN  LAQVR (SEQ ID NO:2)

```

FEATURES:

Functional domains and key regions:

Prosite results:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

1005-1008 NLS

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 2

1 872-875 RKFS
2 1084-1087 RKWS

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 23

1 97-99 STR
2 152-154 SEK
3 156-158 SHR
4 230-232 TRK
5 364-366 SDR
6 450-452 SYK
7 536-538 SER
8 588-590 SRR
9 668-670 TPR
10 762-764 SCK
11 827-829 SLR
12 870-872 TMR
13 947-949 SAR
14 1147-1149 SFR

FIGURE 2A

15 1203-1205 SSR
16 1211-1213 TLK
17 1310-1312 TSK
18 1320-1322 TFR
19 1365-1367 STK
20 1391-1393 SGR
21 1434-1436 SPR
22 1521-1523 SDK
23 1638-1640 TAR

[4] PDOC00006 PS00006 CK2 PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 21

1 59-62 TIED
2 163-166 SFYE
3 242-245 SSEE
4 257-260 TEAE
5 312-315 TPAE
6 459-462 SIPE
7 491-494 SSSD
8 493-496 SDNE
9 528-531 SLPE
10 762-765 SCKE
11 915-918 SQSE
12 929-932 SQSE
13 917-920 SEEE
14 1351-1354 SEEE
15 915-918 SQSE
16 929-932 SQSE
17 961-964 SSPE
18 966-969 TPWE
19 997-1000 SEVD
20 1336-1339 SPSE
21 917-920 SEEE

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 27

1 7-12 GCGGCS
2 10-15 GCSVAH
3 41-46 GGLHSS
4 42-47 GLHSSL
5 106-111 GTTYSL
6 122-127 GVYTCL
7 133-138 GQVLCK
8 484-489 GGSSSS
9 485-490 GSSSSS
10 601-606 GGYIAG
11 606-611 GALPGL
12 708-713 GGHPGT
13 877-882 GGRGGY
14 880-885 GGYAGV
15 894-899 GGDAGG
16 898-903 GGMLGQ
17 1061-1066 GLEITE
18 1174-1179 GQSVTL
19 1229-1234 GVYTCS
20 1240-1245 GTVTTT
21 1293-1298 GGSWTT
22 1294-1299 GSWTTL
23 1316-1321 GGTYYTF
24 1508-1513 GNAQSL
25 1575-1580 GLRKGL
26 1589-1594 GLSGGA
27 1592-1597 GGAVAF

FIGURE 2B

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[6] PDOC00009 PS00009 AMIDATION

Amidation site

1080-1083 VGRK

[7] PDOC00373 PS00343 GRAM_POS_ANCHORING

Gram-positive cocci surface proteins 'anchoring' hexapeptide

704-709 LPSTGG

[8] PDOC00100 PS00107 PROTEIN_KINASE_ATP

Protein kinases ATP-binding region signature

171-194 IGRGVFGFVKRVQHKGNKILCAAK

[9] PDOC00100 PS00108 PROTEIN_KINASE_ST

Serine/Threonine protein kinases active-site signature

280-292 VLHLDIKPSNILM

[10] PDOC00100 PS00109 PROTEIN_KINASE_TYR

Tyrosine protein kinases specific active-site signature

1484-1496 ILHLDLRSENMI

[11] PDOC00565 PS00659 GLYCOSYL_HYDROL_F5

Glycosyl hydrolases family 5 signature

142-151 LVLGGDNEPD

BLAST Alignment to Top Hits:

>gi|7242949|dbj|BAA92535.1| (AB037718) KIAA1297 protein [Homo sapiens]
Length = 2242

Score = 425 bits (1081), Expect = e-117

Identities = 305/876 (34%), Positives = 423/876 (47%), Gaps = 106/876 (12%)

Query: 54 PSMQVTIEDVQAQTGGTAQFEAIIIEGDPQPSVTWYKDSVQLVDSTRLSQQEGTTSYSLVL 113
P + +EDV+ G TA+F ++EG P P + WYKD V L +S+ +S E SLV+
Sbjct: 504 PRFESIMEDVEVGAGETARFAVVVEGKPLPDIMWYKDEVLLTESSHVSFVYEENECSLVV 563

Query: 114 RHVASKDAGVYTCLAQNTGGQVLCKAELLVLGGDN----EPDSEKQSHR-RKLHSFYEVK 168
++D GVYTC AQN G+V CKAE L V E E + HR R+L FY++
Sbjct: 564 LSTGAQDGGVYTCTAQNLAGVSCKAELAVHSAQTAMEVEGVEDEHRRRLSDFYDIH 623

Query: 169 EEIGRGVFGFVKRVQHKGNKILCAAKFIPLRSRTRAQAYRERDILAALSHPLVTGLLDQF 228
+EIGRG F +++R+ + + + AAKFIP +++ +A A RE +LA L H V + F
Sbjct: 624 QEIGRGAFSYLRRIVERSSGLEFAAKFIPSAKPKASARREARLLARLQHDCVLYFHEAF 683

Query: 229 ETRKTLILILELCSSEELLDRLYRKGVVTEAEVKVYIQQQLVEGLHYLHSHGVLHLDIKPS 288
E R+ L+++ ELC+ EELL+R+ RK V E+E++ Y++Q++EG+HYLH VLHLD+KP
Sbjct: 684 ERRRGLVIVTELCT-EELLERIARKPTVCESEIRAYMRQVLEGIHYLHQSHVLHLDVKPE 742

Query: 289 NILMVHPA--REDIKICDFGFAQNITPAELQFSQYGSPEFVSPEIIQNPVSEASDIWAM 346
N+L+ A + ++ICDFG AQ +TP E Q+ QYG+PEFV+PEI+ Q+PVS +DIW +
Sbjct: 743 NLLVWDGAAGEQQVRICDFGNAQELTPGEPQYCYGTPEFVAPEIVNQSPVSGVTDIWPV 802

Query: 347 GVISYLSLTCSPPFAGESDRATLLNVLEGRVSWSSPMAAHLSEDAKDF-IKATLQRAPQA 405
GV+++L LT SPF GE+DR TL+N+ V++ LS +A+ F IK +Q +
Sbjct: 803 GVVAFCLCTGISPFVGENDRITLMNIRYNVAFEEITFLSLREARGFLIKVLVQ--DRL 860

Query: 406 RPSAAQCLSHPWFLKSMPEAEAHFINTKQLKFLARSRWQSLMSYKSILVMRSIPELLR 465
RP+A + L HPWF E ++T LK L+R RWQRS +SYK LV+R IPELLR
Sbjct: 861 RPTAETLEHPWFKTQAKGAE---VSTDHLKFLSRRRWQRSQISYKCHLVLRPIPELLR 917

Query: 466 GPPDSPSLGVARHLCRDTGGSSSSSSSSSDNELAPFARAK-----SLPPSPVTH 513
PP+ + + R +GG SSSS S + EL SL P
Sbjct: 918 APPERVVWTPRR-PPPSGGLSSSSDSEEELEELPSVPRPLQPEFSGSRVSLTDIPTED 976

Query: 514 SPLLHPRGFLRPSASLPPEAEASERSTEAPAPPASPEGAGPPAAQGCVPRHHSVI----- 567

FIGURE 2C

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L P E+ A + EAP+P A P PAA G PR +
Sbjct: 977 EALGTPETGAATPMDWQEQGRAPSDQDEAPSPEALPSPGQEPAA-GASPRRGELRRGSSA 1035
Query: 568 -----RSLFYHQAGESPEHGALAPG-----SRRHPARRRHLLK 600
R L + E P+ + PG ++R A R+ LL+
Sbjct: 1036 ESALPRAGPRELGRGLHKAASVELPQRRSPGPGATRLARGGLGEGEYARLQALRQRLLR 1095
Query: 601 GGYIAGALPGLREPLMEH-----RVLEEEAAREEQATL----LAKAPSFETALR 645
GG G + GLR PL+E R EAA Q L L K+ SF
Sbjct: 1096 GGPEDGKVSGLRGPLLESGLGRARDPRMARASSEAAPHHPPLENRGLQKSSFSQGEA 1155
Query: 646 LPASGTHLAPGHSLSLEHDSPTPR----PSSEACGEAQLPSAPSGGAPIRDMGHPOGS 701
P G H G + R PS A EAQ PS+P+ P
Sbjct: 1156 EP-RGRHRRAGAPLEIPVARLGARRLQESPSLSALSEAQ--PSSPA-----RPSAP 1203
Query: 702 KQLPSTGGHPGTAQPERPSPDSPWGPAPFCHPKQGSAPQEGCSHPAVAPCPP---GS 757
K PST P +A+P +P PAP P Q AP+ P A P PP +
Sbjct: 1204 K--PST---PKSAEPSATTPSDAPQPPAP--QPAQDKAPEPRPEPVRASKPAPPPQALQT 1256
Query: 758 FPPGSCKEAPLVFPSSPFLGQPQAPPAPAKASPLDSKMGPGDISLPGRPKPGPCSSPGSA 817
A ++ S G Q P+ A+PP + K + P PG +
Sbjct: 1257 LALPLTPYAQIIQSLQLSGHAQG-PSQGPAAAPPSEPKPHAAVFARVASPPPG--APEKRV 1313
Query: 818 SQASSSQVSSLRVGSSQVGTPEPGPSLDAEGWTQEA 853
A V + + V PG SL + E+E
Sbjct: 1314 PSAGGPPVLAEKARVPTVPPRPGSSSLSSSIENLESE 1349 (SEQ ID NO:4)

Score = 210 bits (529), Expect = 1e-52

Identities = 111/281 (39%), Positives = 156/281 (55%), Gaps = 2/281 (0%)

Query: 1336 SPSEQVLLGGPSHLASEEESQGRSAQLPSTKTFAFQTQIQGRFVSVRQCWEKASGRAL 1395
SP+++V+ S S +G ++ P K + F + RGRF VVR C E A+GR
Sbjct: 1952 SPAKEVSSSPGSSPRSSPRPEGTTLRQGPQKPYTFLEEKARGRFGVVRACRENATGRTF 2011
Query: 1396 AAKIIPYHPKDKTAVLREYEALKGLRHPHLAQLHAAYLSPRHLVLILELCSGPELLPCLA 1455
AKI+PY + K VL+EYE L+ L H + LH AY++PR+LVLI E C ELL L+
Sbjct: 2012 VAKIVPYAAEGKPRVLQYEYEVRLTLHHERIMSLHEAYITPRYLVLIAESCGNRELLCGLS 2071
Query: 1456 ERASYSESEVKDYLMQMSLATQYLHNQHILHLDLRSENMIITEYNLLKVVDLGNAQSLSQ 1515
+R YSE +V Y+ Q+L YLH H+LHLD++ +N+++ N LK+VD G+AQ +
Sbjct: 2072 DRFRYSEDDVATYMVQLLQGLDYLGHHVHLHLDIKPDNLLAPDNALKIVDFGSAQPYNP 2131
Query: 1516 EKVLPSPDKFKDYLETMAPELLEGQGAVPQTDIWAIGVTAFIMLSAEYPVSSEGARDLQRG 1575
+ + P LE MAPE+++G+ TDIW GV +IMLS P ++ +
Sbjct: 2132 QALRPLGHRTGTLEFMAPEMVKGEPISATDIWGAGVLTYYIMLSGRSPFYEPDPQETEAR 2191
Query: 1576 LRKGLVRLSRCYAGLSGGAVAFLRSTLCAQPWGRPCASSCL 1616
+ G + Y S A FLR L PW RP SSCL
Sbjct: 2192 IVGGRFADFQLYPNTSQSATLFLRKVLSVHPWSRP--SSCL 2230 (SEQ ID NO:5)

Score = 170 bits (426), Expect = 1e-40

Identities = 168/574 (29%), Positives = 256/574 (44%), Gaps = 42/574 (7%)

Query: 1103 LDEP--AELGLRERVKASVEHISRLKGRPEGLEKEGPPRKKPGLASFRLSGLKSWDRAP 1160
L EP A GLR+ V+HI R+L + K PP + L L + + AP
Sbjct: 358 LREPGWAATGLRK----GVQHIFRVLSTTVKSSSKPSPSEPVL----LEHGPTLEEAP 409
Query: 1161 TFLRELSDETIVVLGQSVTLACQVSAQPAQAATW-SKDGAPLESSSRVL-ISATLKNFQLL 1218
L + VV GQ ++ + AQ W S GA LE+ + V +S + L
Sbjct: 410 AMLDKPDIVYVVEGQPASVTVTFN-HVEAQVVWRSCRGALLEARAGVYELSQPDDQYCL 468
Query: 1219 TILVVVAEDLGVTCSVSNALGTVTTTGVLRKAERPS-SSPCDI----GEVYADGVLLV 1273
I V D+G TC+ N GT T + L AE P S D+ GE V++
Sbjct: 469 RICRVSRRDMGALTCTARNRHGTQTCSVTLELAEAPRFESIMEDVEVGAGETARFAVVVE 528
Query: 1274 WKPVESYGPVTYIVQCSLEGGSWTTLASDIFDCCY--LTSKLSRGGTYTFRACVSKAGM 1331
KP+ + Y + L S + + +C L++ GG YT C ++
Sbjct: 529 GKPLPDI--MWYKDEVLLTESSHVSFVYEENECSLVVLSTGAQDGGVYT----CTAQNLA 582

FIGURE 2D

Docket No.: CL000927-CIP-DIV2
Serial No.: To be assigned
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN KINASE PROTEINS...

Query: 1332 GPYSSPSEQVLLGGPSHLASEEESQGRSAQPLPSTKTFAFQTQIQGRFSVVRQCWEKAS 1391
G S +E + + + E + + + + +I RG FS +R+ E++S
Sbjct: 583 GEVSCKAELAVHSAQTAMEVEGVGEDEDHRGRRLSDFYDIHQEIGRGAFSYLRRIVERSS 642

Query: 1392 GRALAAKIIPYHPKDKTAVLREYEALKGLRHPHLAQLHAAYLSPRHLVLILELCSGPELL 1451
G AAK IP K K + RE L L+H + H A+ R LV++ ELC+ ELL
Sbjct: 643 GLEFAAKFIPSAKPKASARREARLLARLQHDCLVLFHEAFERRRGLVIVTELCT-EELL 701

Query: 1452 PCLAERASYSESEVKDYWLQMLSATQYLHNQHILHLDLRSENMIITE---YNLLKVVDL 1507
+A + + ESE++ Y+ Q+L YLH H+LHLD++ EN+++ + + + D
Sbjct: 702 ERIARKPTVCESEIRAYMRQVLEGIHYLHQSHVLHLDVVKPENLLVWDGAGEQQVRICDF 761

Query: 1508 GNAQSLSQEKVLPSPDKFKDYLETMAPELLEGQAVPQTDIWAIGVTAFIMLSAEYPVSSE 1567
GNAQ L+ + P E +APE++ TDIW +GV AF+ L+ P E
Sbjct: 762 GNAQELTPGE--PQYCYGTPEFVAPAEIVNQSPVSGVTDIWPVGVVAFCLCTGISPFVGE 819

Query: 1568 GARDLQRLRGLRGLVRLSR-CYAGLSGGAVAFRLSTLCAQPWGRPCASSCLQCPWLTEEGP 1626
R +R V + LS A FL L Q RP A L+ PW +
Sbjct: 820 NDRITLMNIRNYNVAFEETFLSLSRREARGFLIKVL-VQDRLRPTAETLEHPWFKTQ-- 876

Query: 1627 ACSRPAPVTFPTARLRVFFV-RNREKRRALLYKRH 1659
++ A V+ T L++F+ R R +R + YK H
Sbjct: 877 --AKGAEVS--TDHLKFLSRRRWQRSQISYKCH 906 (SEQ ID NO:6)

Score = 145 bits (362), Expect = 4e-33
Identities = 85/253 (33%), Positives = 135/253 (52%), Gaps = 5/253 (1%)

Query: 165 YEVKEEIGRGVGFVKRVQHKGNILCAAKFIPLRSRTAQAYRERDILAALSHPLVTGL 224
Y EE RG FG V+ + AK +P + + + +E ++L L H + L
Sbjct: 1985 YTFLEEKARGRFGVVRACRENATGRFTVAKIVPYAAEGKPRVLQYEYEVLRTLHHERIMSL 2044

Query: 225 LDQFETRKTLLILELCSSEELLDRLYRKGVVTEAEVKVYIQLVEGLHYLHSHGVHLHD 284
+ + T + L+LI E C + ELL L + +E +V Y+ QL++GL YLH H VLHLD
Sbjct: 2045 HEAYITPRYLVLIAESCGNRELLCGLSDRFRYSEDDVATYMQLLQGLDYLHGHVHLHD 2104

Query: 285 IKPSNIMVHPAREDIKICDFGFAQNTPAELQ--FSQYGSPEFVSPEIIQNPVSEASD 342
IKP N+L+ +KI DFG AQ P L+ + G+ EF++PE+++ P+ A+D
Sbjct: 2105 IKPDNLLLA--PDNALKIVDFGSAQYPNPQALRPLGHRTGTLEFMAPEMVKGEPFISATD 2162

Query: 343 IWAMGVISYLSLTSSPFAGESDRATLLNVLEGRVSWSSPMAAHLSEDAKDFIKATLQRA 402
IW GV++Y+ L+ SPF + T ++ GR + + + S+ A F++ L
Sbjct: 2163 IWGAGVLTYIMLSGRSPFYEPDPQETEARIVGGRFD-AFQLYPNTSQSATLFLRKVLSVH 2221

Query: 403 PQARPSAAQCLSH 415
P +RPS+ + H
Sbjct: 2222 PWSRPSSCLSVCH 2234 (SEQ ID NO:7)

Score = 128 bits (319), Expect = 4e-28
Identities = 81/245 (33%), Positives = 120/245 (48%), Gaps = 19/245 (7%)

Query: 1139 PRKKPGLASFRLSGL-----KSWDRAPTFLRELSDETIVLGQSVTLACQVSAQP 1187
PRK GL+ LS D P F +L D+ ++ G++ TL C +A P
Sbjct: 1571 PRKDKGLSPPNLSASVQEELGHQYVRSEDFPPVFHIKLDQVLLEGEAATLLCLPAACP 1630

Query: 1188 AAQATWSKDGAPLESSSRVLISATLKNFQLLTILVVVAEDLGVTCSVSNALGTVTTTGV 1247
A +W KD L S V+I + QLL+I G+Y CS +N LG++T++
Sbjct: 1631 APHISWMKDKSLRSEPSVIIIVSCKDGRQLLSIPRAGKRHAGLYECSATNVLSITSSCT 1690

Query: 1248 LRKAERPSSSPCPDIGEVYADGVLLVWKPVESYGPVTYIVQCSLEGGG-WTTLASDIFDC 1306
+ A P P++ + Y D L++WKP +S P TY ++ ++G S W ++S I DC
Sbjct: 1691 VAVARVPGKLAPPEVTQTYQDTALVLWKPGRAPCTYTLERRVDGESVWHVPVSSGIPDC 1750

Query: 1307 CYLTSKLSRGGTYTFRACVSKAGMGPYSSPSEQVLLGG-----PSHLASEEESQGRS 1359
Y + L G T FR AC ++AG GP+S+ SE+V + G PS E R
Sbjct: 1751 YYNVTHLPVGVTVRFRVACANRAGQGPFSNSSEKVFVRGTQDSSAVPSAAHQEAPVTSRP 1810

Query: 1360 AQPLP 1364

FIGURE 2E

Docket No.: CL000927-CIP-DIV2
Serial No.: To be assigned
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN KINASE PROTEINS...

A+ P
Sbjct: 1811 ARARP 1815 (SEQ ID NO:8)

Score = 71.0 bits (171), Expect = 9e-11
Identities = 41/115 (35%), Positives = 57/115 (48%), Gaps = 4/115 (3%)

Query: 60 IEDVQAQTGGTAQFEAIEGDPQPSVTWYKDSVQLVDSTRLSQQQEGTTYSLVLRHVASK 119
+EDV+ G A+F+ I G P P VTW + +S L +Q+G +SL + HV S+
Sbjct: 89 LEDVEVLEGRAARFDCKISGTPPPVVTWTHFGCPMEESLRLRQDGGGLHSLHIAHVGSE 148

Query: 120 DAGVYTCLAQNTGGQVLCKAELLVLGGDNEPDSEKQSHRRKLHSFYEVKEEIGRG 174
D G+Y A NT GQ C A+L V EP + KL + EE +G
Sbjct: 149 DEGLYAVSAVNTHGQAHCSAQLYV----EEPRTAASGPSSKLEKMPISPEEPEQG 199 (SEQ ID NO:9)

Score = 60.1 bits (143), Expect = 2e-07
Identities = 54/199 (27%), Positives = 81/199 (40%), Gaps = 12/199 (6%)

Query: 1160 PTFLELSDETIVVLGQSVTLACQVSAQPAQATWSKDGAPLESSSRVLISATLKNFQLLT 1219
P FLR L D V L + L CQV+ P +W +G ++SS ++ ++ L
Sbjct: 207 PDFLRPLQDLEVLGAKEAMLECCQVTGLPYPTISWFHNGHRIQSSDDRRMT-QYRDVHRLV 265

Query: 1220 ILVVVAEDLGVYTCSVSNALGTVTTTGVLRKAERPSSSP--CPDIGEVYADGVLLVWKPV 1277
V + G V Y ++N LG L + P P + V V L W P
Sbjct: 266 FPAVGPQHAGVYKSVIANKLGAACYAHLYVTDVVPGPDPGAPQVAVTGRMVTLTWNPP 325

Query: 1278 ESY-----GPVTYIVQCSLEGG-SWTTLASDIFDCCYLTSKLSRGGTYTFRACVSKAG 1330
S +TY VQ + G WT L + + + + + L +G + FR +
Sbjct: 326 RSLDMAIDPDSLTYTVQHQLGSDQWTALVTGLREPGWAATGLRKGVQHIFRVLSTTVKS 385

Query: 1331 MGPYSSPSE--QVLLGGPS 1347
S PSE Q+L GP+
Sbjct: 386 SSKPSPSPSEPVQLLEHGPT 404 (SEQ ID NO:10)

Score = 45.7 bits (106), Expect = 0.004
Identities = 30/102 (29%), Positives = 45/102 (43%), Gaps = 1/102 (0%)

Query: 1159 APTFLRELSDETIVVLGQSVTLACQVSAQPAQATWSKDGAPLESSSRVLISATLKNFQLL 1218
AP F R L D V+ G++ C++S P TW+ G P+E S + + L
Sbjct: 82 APLFTRLEDVEVLEGRAARFDCKISGTPPPVVTWTHFGCPMEESLRLRQD-GGLHSL 140

Query: 1219 TILVVVAEDLGVYTCSVSNALGTVTTTGVLRKAERPSSSPCP 1260
I V +ED G+Y S N G + L E +++ P
Sbjct: 141 HIAHVGSEDEGLYAVSAVNTHGQAHCSAQLYVEEPRTAASGP 182 (SEQ ID NO:11)

Score = 43.8 bits (101), Expect = 0.015
Identities = 58/217 (26%), Positives = 84/217 (37%), Gaps = 23/217 (10%)

Query: 619 RVLEEEAAREEQATLLAKAPSFETALRLPASGTHLAPGHSHSLEHDSPTPRPSSEACGE 678
R ++ +A A A S R P S T LAP + + T PSS
Sbjct: 1788 RGTQDSSAVPSAAHQEAPVTSRPARAPPDSPSTLAPPLAPAAPTPPSVTVPSSSPPTPP 1847

Query: 679 AQRLPSPAPSGGAPIRDMGHPQGSKQLPSTGGHPGTAQPERPSPDPSWGQAPAPFCHPKQGS 738
+Q L S + G P + P+ + L + A+P PS +P PF
Sbjct: 1848 SQALSSLKAVGPPPTQTP--PRRHRLQAAR----PAEPTLPSTHVTPEPKPFVLD---- 1897

Query: 739 APQEGCSPHAPAVAPCPPGSPGSCKEAPLVPSSPFLGQPQAPPAPAKASPPLDKMGPG 798
+ P A P G P S P+ + F+ P AP PA PP +K+
Sbjct: 1898 -----TGTFIPASTPQGVKPVSS--STPVYVVTSFVSAPPAPEPPAPEPPPEPTKVTQV 1949

Query: 799 DISLPGRPKPGPCSSPGSASQAS-SSQVSSLRVGSSQ 834
+S P SSPGS+ ++S + ++LR G Q
Sbjct: 1950 SLS-----PAKEVVSSPGSSPRSSPRPEGTTLRQGPPQ 1982 (SEQ ID NO:12)

Score = 43.0 bits (99), Expect = 0.026
Identities = 25/92 (27%), Positives = 44/92 (47%), Gaps = 4/92 (4%)

FIGURE 2F

Docket No.: CL000927-CIP-DIV2
Serial No.: To be assigned
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN KINASE PROTEINS...

Query: 54 PSMQVTIEDVQAQTGGTAQFEAIEGDPQPSVTWYKDS--VQLVDSTRLSQQQEGTTYSL 111
P ++D++ A E + G P P+++W+ + +Q D R++Q ++ + L
Sbjct: 207 PDFLRPLQDLEVLAKEMLEQCQTGLPYPTISWFHNGHRIQSSDDRRMTQYRD--VHRL 264

Query: 112 VLRHVASKDAGVYTCLAQNTGGQVLCKAELLV 143
V V + AGVY + N G+ C A L V
Sbjct: 265 VFPAVGPPHAGVYKSVIANKLGAACYAHLV 296 (SEQ ID NO:13)

>gi|8928460|sp|O75962|TRIO_HUMAN TRIPLE FUNCTIONAL DOMAIN PROTEIN
(PTPRF INTERACTING PROTEIN) >gi|3644048|gb|AAC43042.1|
(AF091395) Trio isoform [Homo sapiens]
Length = 3038

Score = 229 bits (579), Expect = 1e-58
Identities = 143/418 (34%), Positives = 215/418 (51%), Gaps = 11/418 (2%)

Query: 53 PPSMQVTIEDVQAQTGGTAQFEAIEGDPQPSVTWYKDSVQLVDST---RLSQQQEGTTY 109
PP + + +V +TG T + G P+ S+TW +++ +S G
Sbjct: 2625 PPEFVLIPLSEVTCETGETVVLRCRVCGRPKASITWKGPENHTLNNDGHYSISYSDLGAE- 2683

Query: 110 SLVLRHVASKDAGVYTCLAQNTGGQVLCKAELLVLLGGDNEPDSEKQSHRRKLHSFYEVKE 169
+L + V ++D G+YTC+A N G A L VLG D + + SFY
Sbjct: 2684 TLKIVGVTTEDDGIYTCIAVNDMGSASSASLRVLGPGM--DGIMVTWKDNFDSFYSEVA 2741

Query: 170 EIGRGVFGFVKRVQHKGNKILCAAKFIPLRSRTRAQAYRERDILAALSHPLVTGLLDQFE 229
E+GRG F VK+ KG K A KF+ + R Q E IL +L HPL+ GLLD FE
Sbjct: 2742 ELGRGRFSVVKCDQKGTKRAVATKFNKKLMKRDQVTHELGILQSLQHPLLVGLLDTFE 2801

Query: 230 TRKTLILILELCSSEELDLRLYRKGVTTEAEVKVYIQQLVLEGLHYLHSHGVLHLDIKPSN 289
T + IL+LE+ LLD + R G +TE +++ ++ ++E + YLH+ + HLD+KP N
Sbjct: 2802 TPTSYILVLEMAHQGRLLDCVVRWGSLETKIRAHLEGEVLEAVRYLHNCRIAHLDLKPEN 2861

Query: 290 ILMVHP-AREDIKICDFGFAQNITPAELQFSQYGSPEFVSPEIIQQNPVSEASDIWAMGV 348
IL+ A+ IK+ DFG A + G+PEF +PEII NPVS SD W++GV
Sbjct: 2862 ILVDESIAKPTIKLADFGDAVQLNTTYIHLGNPEFAAPEIILGNPVSLTSDTWSVG 2921

Query: 349 ISYLSLTCSPPFAGESDRATLLNVLEGRVSWSSPMAAHLSEDAKDFIKATLQRAQARPS 408
++Y+ L+ SPF +S T LN+ S+ +S+ AK+F+ LQ P RPS
Sbjct: 2922 LTYVLLSGVSPFLDDSVETCLNICRLDFSFPDDYFKGVSQKAKEFVCFLQEDPAKRPS 2981

Query: 409 AAQCLSHPWFLKSMPAAEEAHFINTKQLKFLARSRWQ---RSLMSYKSILVMRSIPEL 463
AA L W L++ ++T+L + R + Q R + S K+ L R +P +
Sbjct: 2982 AALALQEQW-LQAGNGRSTGVLDTSRLTSFIERRKHQNDVRPIRSIKNFLQSRLPRV 3038
(SEQ ID NO:14)

Score = 121 bits (300), Expect = 7e-26
Identities = 82/280 (29%), Positives = 137/280 (48%), Gaps = 10/280 (3%)

Query: 1374 QIQRGRFSVVRQCWEKASGRALAAKIIPYHPKDKTAVLREYEALKGLRHPHLAQLHAAAYL 1433
++ RGRFSV++C +K + RA+A K + + V E L+ L+HP L L +
Sbjct: 2742 ELGRGRFSVVKCDQKGTKRAVATKFNKKLMKRDQVTHELGILQSLQHPLLVGLLDTFE 2801

Query: 1434 SPRHLVLILELCSGPELLPCLAERASYSESEVKDYLVQMLSATQYLHNQHILHLDLRSN 1493
+P +L+LE+ LL C+ S +E +++ +L ++L A +YLHN I HLDL+ EN
Sbjct: 2802 TPTSYILVLEMAHQGRLLDCVVRWGSLETKIRAHLEGEVLEAVRYLHNCRIAHLDLKPEN 2861

Query: 1494 MIITE---YNLLKVVDLGNAQSLSQEKVLPSPDKFKDYLETMAPELLEGQGAVPQTDIWI 1550
+++ E +K+ D G+A L+ + + E APE++ G +D W++
Sbjct: 2862 ILVDESIAKPTIKLADFGDAVQLNTTYI--HQLLGNPEFAAPEIILGNPVSLTSDTWSV 2919

Query: 1551 GVTAFIMLSAEYPVSSEGARDLQRL-RKGLVRLSRCYAGLSGGAVAFRLSTLCAQPWGR 1609
GV +++LS P + + + R + G+S A F+ L P R
Sbjct: 2920 GVLTYVLLSGVSPFLDDSVETCLNICRLDFSFPDDYFKGVSQKAKEFVCFLQEDPAKR 2979

Query: 1610 PCASSCLQCPWLTEEGPACSRPAPVTFPTARLRFVVRNRE 1649
P A+ LQ WL A + + T+RL F+ R+
Sbjct: 2980 PSAALALQEQWL---QAGNGRSTGVLDTSRLTSFIERRK 3015 (SEQ ID NO:15)

FIGURE 2G

Dock t No.: CL000927-CIP-DIV2
Serial No.: To b assigned
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN KINASE PROTEINS...

Score = 55.4 bits (131), Expect = 5e-06
Identities = 42/153 (27%), Positives = 70/153 (45%), Gaps = 17/153 (11%)

Query: 1128 GRPEGLEKEGPPRKKPGLASFRLSGLKS---WDRAPTFLRELSDET VVLGQSVTLACQV 1183
G+ EG + G + + GL++ L + +D P F+ LS+ T G++V L C+V
Sbjct: 2590 GKREGKLENGYRKSREGLSNKVSVKLLNPNIYDVPPEFVIPLSEVTCETGETTVVLRRCRV 2649

Query: 1184 SAQPAAQATW-SKDGAPESSSRVLISATLKNFQLLTILVVVAEDLGVTCSVSNALGTV 1242
+P A TW + L + IS + L I+ V ED G+YTC N +G+
Sbjct: 2650 CGRPKASITWKGPENHTLNNDGHYSISYSDLGEATLKIVGVTTEDDGIYTCIAVNDMGSA 2709

Query: 1243 TTTGVLKRAERPSSSPCPDIGEVYADGVLLVWK 1275
+++ LR + DG+++ WK
Sbjct: 2710 SSSASLR-----VLGPGMDGIMVTWK 2730 (SEQ ID NO:16)

Score = 39.1 bits (89), Expect = 0.39
Identities = 61/208 (29%), Positives = 76/208 (36%), Gaps = 65/208 (31%)

Query: 688 GGAPIRDMGHPQGSKQLPSTGGHPGTA-----QPERPSPD-----S 723
GGAP GH G S GG P T+ QP R P S
Sbjct: 2252 GGAPSGGSGHSGGPS---SCGGAPSTSRSRPSRIPQPVRRHPPVLVSSAASSQAEADKMS 2308

Query: 724 PWGQPAFPCHPKQGSAPQEGCSPHPAVAPCPGSPFPGSCKEAPLVSSPFLGQPQ---- 779
P P P G+AP+ G S A + PPG+ GS +EA +P L P+
Sbjct: 2309 GTSTPGPSL-PPGAAPEAGPS---APSRPPGADAEGSERAEPKMKVLES PRKGAA 2364

Query: 780 -----APPAPAK-----ASPPLDSKMGPDISLPGRPKPGPCSSPGSA 817
+P APAK A+ PL+S + SL P P P S
Sbjct: 2365 NASGSSPDAPAKDARASLGTLPLGKPRAGAASPLNSPLSSAVPSLGKEPFP-----PSSP 2419

Query: 818 SQASSSQVSSLRVG-SSQVG--TEPGPS 842
Q S SS+ +S+ G T PG S
Sbjct: 2420 LQKGGFWSSIPASPARPGSFTFP GD S 2447 (SEQ ID NO:17)

>gi|3024081|sp|Q15746|KMLS_HUMAN MYOSIN LIGHT CHAIN KINASE, SMOOTH
MUSCLE AND NON-MUSCLE ISOZYMES (MLCK) [CONTAINS: TELOKIN]
Length = 1913

Score = 206 bits (518), Expect = 2e-51
Identities = 104/298 (34%), Positives = 173/298 (57%), Gaps = 2/298 (0%)

Query: 159 RKLHSFYEVKEEIGRGVFGVFKRVQHKGNKILCAAKFIPLRSRTRAQAYRER-DILAALS 217
+K+ FY+++E +G G FG V R+ K + + A KF S + R+ I+ L
Sbjct: 1458 QKVSDFYDIEERLGSGKFGQVFRLEKTRKVVAGKFFKAYSACEKENIRQEISIMNCLH 1517

Query: 218 HPLVTGLLDQFETRKTLLILELCSSEBLDLRYRKGV-VTEAEVKVYIQQVLEGLHYLH 276
HP + +D FE + ++++LE+ S EL +R+ + +TE E Y++Q+ EG+ Y+H
Sbjct: 1518 HPKLVQCVDAFEKANIVMVLEIVSGGELFERIIDDEFELTERECIKYMRQISEGVYIH 1577

Query: 277 SHGVLHLDIKPSNIMLVHPAREDIKICDFGFAQNITPAELQFSQYGSPEFVSPEIIQONP 336
G++HLD+KP NI+ V+ IK+ DFG A+ + A +G+PEFV+PE+I P
Sbjct: 1578 KQGIHVLDLKPENIMCVNKTGTRIKLIDFGLARLENAGSLKVLFGTPEFVAPEVINYEP 1637

Query: 337 VSEASDIWAMGVISYLSLTCSPPFAGESDRATLLNVLEGRVSWSSPMAAHLSEDAKDFIK 396
+S A+D+W++GVI Y+ ++ SPF G++D TL NV + +S+DAKDFI
Sbjct: 1638 ISYATDMWSIGVICIYLVSLSPFMGDNDNETLANVTSATWDFDDEAFDEISDDAKDFIS 1697

Query: 397 ATLQRAPQARPSAAQCLSHPWFLKSMPAEEAHFINTKQLKFLARSRWQRLMSYKSI 454
L++ + R QCL HPW +K EA ++ +K +AR +WQ++ + ++I
Sbjct: 1698 NLLKKDMKNRLDCTQCLQHPWLMKDTKNMEAKKLSKDRMKKYMARRKWQKTGNVRAI 1755
(SEQ ID NO:18)

Score = 127 bits (315), Expect = 1e-27
Identities = 134/528 (25%), Positives = 219/528 (41%), Gaps = 55/528 (10%)

Query: 1132 GLEKEGPPRKKPGLASFRLSGLKSWDRAPTFLRELSDET VVLGQSVTLACQVSAQPAAQA 1191
G E + +KKP + + + P ++ D+ V G+SV L +V+
Sbjct: 1215 GTESDATVKKKPAKTPPKAAMP-----PQIIQFPEDQKVRAGESVELFGKVTGTQPITC 1269

FIGURE 2H

Dock t No.: CL000927-CIP-DIV2
 S rial No.: To be assigned
 Inventors: Ming-Hui WEI et al.
 Title: ISOLATED HUMAN KINASE PROTEINS...

Query: 1192 TWSKDGAPLESSSRVLISATLKNFQLLTILVVVAEDLGVTYCSVSNALGT---VTTTGV 1247
 TW K ++ S + + + +N LTIL E G YT V N LG+ V T V
 Sbjct: 1270 TWMKFRKQIQDSEHIKVEN-ENGSKLTILAAARQEHGCGCYLLVENKLGSRQAQVNLT-V 1327

Query: 1248 LRKAERPSSSPCPDIGEVYADGVLLVWKPVESYGPVTYIVQCSLE----GGSWTTLASD 1302
 + K + P+ +PC ++ + + L W SY + + S+E +W LA+
 Sbjct: 1328 VDKPDPFAGTPCAS--DIRSSSLTSLWYG-SSYDGGSAVQSYSIEIWDSANKTWKELAT- 1383

Query: 1303 IFDCCYLTS----KLSRGGTYTFRACVSKAGMPYSSPSEQVLLGGPSHLAS----- 1351
 C TS L Y FR ++ G S SE +G
 Sbjct: 1384 ----CRSTSFNVQDLLPDHEYKFRVRRAINVTSEPSQSELTITVGEKPEEPKMKWRCQT 1439

Query: 1352 ----EESQGRSAQPLPSTKTFAF---QTQIQGRFSVVRQCWEKASGRALAAKIIP-YH 1403
 E E R+ K F + ++ G+F V + EK + + A K Y
 Sbjct: 1440 DDEKEPEVDYRTVTINTEQKVSDFYDIEERLGSQKGFQVFRLEKTRKRVWAGKFFKAYS 1499

Query: 1404 PKDKTAVLREYEALGLRHPHLAQLHAAYLSPRHLVLILELCSGPPELLP-CLAERASYSE 1462
 K+K + +E + L HP L Q A+ ++V++LE+ SG EL + E +E
 Sbjct: 1500 AKEKENIRQEISIMNCLHHPKLQVCVDAFEKANIVMVLEIVSGGELFERIIDDFELTE 1559

Query: 1463 SEVKDYLWQMLSATQYLHNQHILHLDRSENMIITEY--NLLKVVDLQNAQSLSQE---K 1517
 E Y+ Q+ +Y+H Q I+HLDL+ EN++ +K++D G A+ L K
 Sbjct: 1560 RECIKYMRISEGVEYIHKQIGIVHLDLKPENIMCVNKTGTRIKLIDFGLARLENAGSLK 1619

Query: 1518 VLPSPDKFKDYLETMAPELLEGQGAVPQTDIWAIGVTAFIMLSAEYFVSSEGARDLQRGLR 1577
 VL E +APE++ + TD+W+IGV +I++S P + + +
 Sbjct: 1620 VLFGTP-----EFVAPEVINYEPISYATDMWSIGVICIYILVSGLSPFMGDNDNETLANVT 1674

Query: 1578 KGLVRL-SRCYAGLSGGAVAFRLRSTLCAQPWGRPCASSCLQCPWLTEE 1624
 + +S A F+ + L R + CLQ PWL ++
 Sbjct: 1675 SATWDFDDEAFDEISDDAKDFISNLLKDMKNRLDCTQCLQHPWLMKD 1722 (SEQ ID NO:19)

Score = 64.4 bits (154), Expect = 9e-09
 Identities = 36/106 (33%), Positives = 52/106 (48%), Gaps = 4/106 (3%)

Query: 54 PSMQVTIEDVQAQTGGTAQFEAIIIEGDPQPSVTWYKDSVQLVDSTRLS-QQEGTTYSLV 112
 P TI D++ G A+F+ IEG P P V W+KD + +S E SL+
 Sbjct: 1808 PYFSKTIIRDLEVVEGSAARFDCKIEGYPDPEVWVFKDDQSIRESRHFQIDYDEDGNCCLI 1867

Query: 113 LRHVASKDAGVYTCLAQNTGGQVLCKAELLV---LGGDNEPDSEKQ 155
 + V D YTC A N+ G+ C AEL+V G+ E + E++
 Sbjct: 1868 ISDVCGDGDDAKYTCVAVNSLGEATCTAELIVETMEEGEGEGESEEEEE 1913 (SEQ ID NO:20)

Score = 64.0 bits (153), Expect = 1e-08
 Identities = 35/96 (36%), Positives = 46/96 (47%)

Query: 53 PPSMQVTIEDVQAQTGGTAQFEAIIIEGDPQPSVTWYKDSVQLVDSTRLSQQEGTTYSLV 112
 PP + V + G +F I G P P V W+K +V L S R+S ++ L
 Sbjct: 160 PPKFATKLRVGVVKEGQMGFRFSCKITGRPPQVTLKGNVPLQPSARVSVSEKNGMQVLE 219

Query: 113 LRHVASKDAGVYTCLAQNTGGQVLCKAELLVLGGDN 148
 + V D GVTCL N G+ AEL + G D+
 Sbjct: 220 IHGVNQDDVGVTCLVNVGSGKASMSAELSIQGLDS 255 (SEQ ID NO:21)

Score = 59.3 bits (141), Expect = 3e-07
 Identities = 30/100 (30%), Positives = 50/100 (50%), Gaps = 3/100 (3%)

Query: 47 LPALPGPPSMQVTIE---DVQAQTGGTAQFEAIIIEGDPQPSVTWYKDSVQLVDSTRLSQQ 103
 LP P P+ + ++ D++ G + G+P P V W + ++ +S +
 Sbjct: 613 LFLVAPSKEPTAFIFLQGLSDLKVMDSQVTMTVQVSGNPPPEVIWLHNGNEIQESEDHFHE 672

Query: 104 QEGTTYSLVLRHVASKDAGVYTCLAQNTGGQVLCKAELLV 143
 Q GT +SL ++ V +D G YTC A N+ G+V +A L V
 Sbjct: 673 QRGTHSLWIQEVFPEDTGTYTCEAWNSAGEVTRQAVLTV 712 (SEQ ID NO:22)

FIGURE 2I

Docket No.: CL000927-CIP-DIV2

Serial No.: To b assigned

Inventors: Ming-Hui WEI et al.

Title: ISOLATED HUMAN KINASE PROTEINS...

Score = 57.4 bits (136), Expect = 1e-06
Identities = 32/89 (35%), Positives = 46/89 (50%), Gaps = 1/89 (1%)

Query: 1160 PTFLRELSDETIVVLGQSVTLACQVSAQPAQAATWSKDGAPLESSSRVLISATLKNFQLLT 1219
P F +L V GQ +C+++ +P Q TW K PL+ S+RV +S Q+L
Sbjct: 161 PKFATKLGRVVKEGQMGFRFSCKITGRPQPQVTLKGNVPLQPSARVSVSEK-NGMQVLE 219

Query: 1220 ILVVVAEDLGVTCSVSINALGTVTTTGVL 1248
I V +D+GVYTC V N G + + L
Sbjct: 220 IHGVNQDDVGVTCLVVNGSGKASMSAEL 248 (SEQ ID NO:23)

Score = 53.5 bits (126), Expect = 2e-05
Identities = 32/98 (32%), Positives = 46/98 (46%), Gaps = 4/98 (4%)

Query: 1159 APTFLRELSDETIVVLGQSVTLACQVSAQPAQAATWSKDGAPLESSSRVLISATLKNFQLL 1218
AP+F L D V+ GQ L C V P + TW +G P++ + + + L
Sbjct: 513 APSFSSVLKDCAVIEGQDFVLQCSVRGTPVPRITWLLNGQPIQYARSTCEAGVAE----L 568

Query: 1219 TILVVVAEDLGVTCSVSINALGTVTTTGVLKRAERPSS 1256
I + ED G YTC NALG V+ + + E+ SS
Sbjct: 569 HIQDALPEDHGTYTCLAENALQVSCSAWVTVHEKKSS 606 (SEQ ID NO:24)

Score = 53.1 bits (125), Expect = 2e-05
Identities = 37/113 (32%), Positives = 48/113 (41%), Gaps = 1/113 (0%)

Query: 1140 RKKPGLASFRLSGLKSWDRAPTFLRELSDETIVVLGQSVTLACQVSAQPAQAATWSKDGAP 1199
+K + + L S AP FL+ LSD V+ G VT+ QVS P + W +G
Sbjct: 603 KKSSRKSEYLLPVAPSKPTAPIFLQGLSDLKVMDSQVTMTVQVSGNPPPEVIWLHNGNE 662

Query: 1200 LESSSRVLISATLKNFQLLTILVVVAEDLGVTCSVSINALGTVTTTGVLKRAE 1252
++ S L I V ED G YTC N+ G V T VL E
Sbjct: 663 IQESEDHFHEQRGTQHS-LWIEVFPEDTGTYTCEAWNSAGEVRTQAVLTVQE 714 (SEQ ID NO:25)

Score = 51.9 bits (122), Expect = 5e-05
Identities = 34/101 (33%), Positives = 50/101 (48%), Gaps = 2/101 (1%)

Query: 46 SLPALPGPPSMQVTIEDVQAQTGGTAQFEAIEGDPQPSVTWYKDSVQLVDSTR-LSQQQ 104
S+P L P+ + ++ + G TA+FE + G P+P VTW+++ + R L
Sbjct: 26 SMP-LTEAPAFILPPRNLCKIEGATAKFEGRVGRYPEPQVTVHRNGQPITSGGRFLDCG 84

Query: 105 EGTYSVLRLRHVASKDAGVYTCLAQNTGGQVLCKAELLVLG 145
T+SLV+ V +D G YTC A N G EL V G
Sbjct: 85 IRGTFSLVIHAVHEEDRGKYTCATNGSGARQVTVELTVEG 125 (SEQ ID NO:26)

Score = 50.8 bits (119), Expect = 1e-04
Identities = 41/182 (22%), Positives = 65/182 (35%), Gaps = 26/182 (14%)

Query: 1130 PEGLEKEGPPRKKPGLASFRLSGLKSWDRA-----PTFLRELSDETV 1171
P G E++ P +P R GL S D P F + + V
Sbjct: 366 PSGEERKRPAAPRPATFTRQPLGSDVVSKAANRRIPMEGQRDSAFPKEKPSQSQEV 425

Query: 1172 VLQSVTLACQVSAQPAQAATWSKDGAPLESSSRVLISATLKNFQLLTILVVVAEDLGVT 1231
Q+V C+VS P + W +G P+ + L +L D G Y
Sbjct: 426 KENQTVKFRCEVSGIPKEVAWFLEGTVPVRRQEGSIEVYEDAGSHYLCCLKARTRDSGT 485

Query: 1232 TCSVSINALGTVTTTGVLKRAERPSSSPCDIGEVYADGVLLVWKPVESYGPVTYIVQCSL 1291
+C+ SNA G V+ + L+ P V D ++ + +++QCS+
Sbjct: 486 SCTASNAQQVSCSWTLQVERLAVMEVAPSFSSVLKDCAVIEGQ-----DFVLQCSV 537

Query: 1292 EG 1293
G
Sbjct: 538 RG 539 (SEQ ID NO:27)

Score = 50.4 bits (118), Expect = 2e-04
Identities = 26/100 (26%), Positives = 47/100 (47%), Gaps = 3/100 (3%)

FIGURE 2J

Docket No.: CL000927-CIP-DIV2
Serial No.: To be assigned
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN KINASE PROTEINS...

Query: 54 PSMQVTIEDVQAQTGGTAQFEAIIEGDPQPSVTWYKDSVQLVDSTRLSQQQEGTTYSLVL 113
P+ + ++DV G + + DP ++ W + L + + QEG+ S+ +
Sbjct: 1098 PAFKQKLQDVHVAEGKKLLQLQCQVSSDPPATIIWTLNGKTLKTTKFIILSQEGSLCSVSI 1157

Query: 114 RHVASKDAGVYTCLAQNTGGQVLCKAELLVLGGDNEPDSE 153
+D G+Y C+A+N GQ C ++ V D+ P SE
Sbjct: 1158 EKALLEDRGLYKCVAKNDAGQAECSCQVTV---DDAPASE 1194 (SEQ ID NO:28)

Score = 50.0 bits (117), Expect = 2e-04
Identities = 35/125 (28%), Positives = 59/125 (47%), Gaps = 16/125 (12%)

Query: 1154 KSWDRAPTFLRELSDETIVLGQSVTLACQVSAQPAQATWSKDGAPLESSSRVLISATLK 1213
+S AP F ++L D V G+ + L CQVS+ P A W+ +G L+++ +++S
Sbjct: 1092 ESQGTAPAFKQLQDVHVAEGKKLLQLQCQVSSDPPATIIWTLNGKTLKTTKFIILSQE-G 1150

Query: 1214 NFQLLTILVVVAEDLGVYTC-----SVSNALGTVTTTGVLRKAERPSSSP 1258
+ ++I + ED G+Y C +V +A + T K+ RP SS
Sbjct: 1151 SLCSVSIEKALLEDRGLYKCVAKNDAGQAECSCQVTVDDAPASENTKAPEMKSRPKSSL 1210

Query: 1259 CPDIG 1263
P +G
Sbjct: 1211 PPVLG 1215 (SEQ ID NO:29)

Score = 48.0 bits (112), Expect = 8e-04
Identities = 26/87 (29%), Positives = 38/87 (42%)

Query: 1159 APTFLRELSDETIVLGQSVTLACQVSAQPAQATWSKDGAPLESSSRVLISATLKNFQLL 1218
AP F+ + + G + +V P Q TW ++G P+ S R L+ ++ L
Sbjct: 32 APAFILPPRNLCIKEGATAKFEGRVGRYPEPQVTWHRNGQPITSGGRFLDCGIRGTFSL 91

Query: 1219 TILVVVAEDLGVYTCSVSNALGTVTTT 1245
I V ED G YTC +N G T
Sbjct: 92 VIHAVHEEDRGKYTCEATNGSGARQVT 118 (SEQ ID NO:30)

Score = 45.3 bits (105), Expect = 0.005
Identities = 37/140 (26%), Positives = 54/140 (38%), Gaps = 23/140 (16%)

Query: 22 TNHPSMVGCGWHPGLCGWGGGLHSSLPALPGPPSMQVTIEDVQAQTGGTAQFEAIIEGDP 81
+N V C W + L + PS ++D G + + G P
Sbjct: 490 SNAQQQVSCSWTLQV-----ERLAVMEVAPSFSSVLKDCAVIEGQDFVLQCSVRGTP 541

Query: 82 QPSVTWYKDS--VQLVDSTRLSQQQEGTTYSLVLRHVASKDAGVYTCLAQNTGGQVLCKA 139
P +TW + +Q ST E L ++ +D G YTC+A+N GQV C A
Sbjct: 542 VPRITWLLNGQPIQYARSTC-----EAGVAELHIQDALPEDHGTYTCLAENALGQVSCSA 596

Query: 140 ELLVLGGDNEPDSEKQSHRR 159
+ V EK+S R+
Sbjct: 597 WVTV-----HEKKSSRK 608 (SEQ ID NO:31)

Score = 44.5 bits (103), Expect = 0.009
Identities = 26/104 (25%), Positives = 44/104 (42%), Gaps = 7/104 (6%)

Query: 41 GGLHSSLPALPGPPSMQVTIEDVQAQTGGTAQFEAIIEGDPQPSVTWYKDSVQLV-DSTR 99
G S+ P P Q + + T +F + G P+P V W+ + +
Sbjct: 407 GQRDSAPFKFESKPQSQ-----EVKENQTVKFRCEVSGIPKPEVAWFLEGTPVRRQEGS 460

Query: 100 LSQQQEGTTYSLVLRHVASKDAGVYTCLAQNTGGQVLCKAELLV 143
+ ++ ++ L L ++D+G Y+C A N GQV C L V
Sbjct: 461 IEVYEDAGSHYLCLLKARTRDSGTYSCTASNAQQQVSCSWTLQV 504 (SEQ ID NO:32)

Score = 44.1 bits (102), Expect = 0.012
Identities = 26/82 (31%), Positives = 38/82 (45%), Gaps = 1/82 (1%)

Query: 63 VQAQTGGTAQFEAIIEGDPQPSVTWYKDSVQLV-DSTRLSQQQEGTTYSLVLRHVASKDA 121

FIGURE 2K

Docket No.: CL000927-CIP-DIV2

Serial No.: To be assigned

Inventors: Ming-Hui WEI et al.

Title: ISOLATED HUMAN KINASE PROTEINS...

V A G + I GDP P+V W +D L D+ Q ++LVL+ V A
Sbjct: 730 VTASLGQSVLISCAIAGDPFPPTVHWLRDGGKALCKDTGHFEVLQNEVDVFTLVLLKKVQPWHA 789

Query: 122 GVYTCCLAQNTGGQVLCKAELLV 143
G Y L +N G+ C+ L++
Sbjct: 790 GQYEILLKNRVGECSCQVSLML 811 (SEQ ID NO:33)

Score = 43.8 bits (101), Expect = 0.015
Identities = 26/89 (29%), Positives = 35/89 (39%)

Query: 1160 PTFLELSDETIVLGQSVTLACQVSAQPAAQATWSKDGAPLESSSRVLISATLKNFQLLT 1219
P F + + D VV G + C++ P + W KD + S I L
Sbjct: 1808 PYFSKTIRDLEVVEGSAARFDCKIEGYPDPEVVWFKDDQSIRESRHFQIDYDEDGNCSLI 1867

Query: 1220 ILVVVAEDLGVYTCVSNALGTVTTTGV 1248
I V +D YTC N+LG T T L
Sbjct: 1868 ISDVCGDDDAKYTC KAVNSLGEATCTAEL 1896 (SEQ ID NO:34)

FIGURE 2L

Docket No.: CL000927-CIP-DIV2

Serial No.: To be assigned

Inventors: Ming-Hui WEI et al.

Title: ISOLATED HUMAN KINASE PROTEINS...

```
1 CAGCACGAGG AACTCCTTCT GATCACCTGG CCAGCTGAGG TCAGAGTGGG
51 AGAGGCAGTG GTTCCATTGA AGGAGTACTC CTAAGTGTCA GAAGCCTGGG
101 CGGTCAAGAT GGGGTGCTGT CGCTTGGGCT GCGGGGGGTG TTCAGTTGCC
151 CACAGTGTAT CTCAGGGTCT CACCAACCAT CCAAGCATGG TAGGCTGTGG
201 CTGGCACCCA GGGTGTGTG GCTGGGGAGG TGGTCTCCAC AGTTCCCTCC
251 CTGCCCTCCC AGGGCCCCCA TCCATGCAGG TAACCATCGA GGATGTGCAG
301 GCACAGACAG GCGGAACGGC CCAATTTCAG GCTATCATTG AGGGCGACCC
351 ACAGCCTCTG GTGACCTGGT ACAAGGACAG CGTCCAGCTG GTGGACAGCA
401 CCCGGCTTAG CCAGCAGCAA GAAGGCACCA CATACTCCCT GGTGCTGAGG
451 CATGTGGCCT CGAAGGATGC CGGCGTTTAC ACCTGCTCTG CCCAAAACAC
501 TGGTGGCCAG GTGCTCTGCA AGGCAGAGCT GCTGGTGCTT GGGGGGGACA
551 ATGAGCCGGA CTCAGAGAAG CAAAGCCACC GGAGGAAGCT GCACTCCTTC
601 TATGAGGTCA AGGAGGAGAT TGAAGGGGCG GTGTTTGGCT TCGTAAAAAG
651 AGTGACGACG AAAGGAAACA AGATCTTGTG CGCTGCCAAG TTCATCCCCC
701 TACGGAGCAG AACTCGGGCC CAGGCATACA GGGAGCGAGA CATCCTGGCC
751 GCCTGAGGCC ACCCGCTGGT CACGGGGCTG CTGGACCACT TTGAGACCCG
801 CAAGACCCTC ATCCTCATCC TGGAGCTGTG CTCATCCGAG GAGCTGCTGG
851 ACCGCTGTGA CAGGAAGGGC GTGGTGACGG AGGCCGAGGT CAAGGTCTAC
901 ATCCAGCAGC TGGTGGAGGG GCTGCACTAC CTGCACAGCC ATGGCGTTCT
951 CCACCTGGAC ATAAAGCCCT CTAACATCCT GATGGTGCAT CCTGCCCGGG
1001 AAGACATTAA AATCTGCGAC TTTGGCTTTG CCCAGAACAT CACCCAGCA
1051 GAGCTGCAGT TCAGCCAGTA CGGCTCCCCT GAGTTCGTCT CCCCCGAGAT
1101 CATCCAGCAG AACCTGTGA GCGAAGCCTC CGACATTTCG GCCATGGGTG
1151 TCATCTCCTA CCTCAGCCTG ACCTGCTCAT CCCCATTTGC CGGCGAGAGT
1201 GACCGTGCCA CCCTCCTGAA CGTCTGGAG GGGCGCGTGT CATGGAGCAG
1251 CCCCATGGCT GCCCACCTCA GCGAAGACGC CAAAGACTTC ATCAAGGCTA
1301 CGCTGCAGAG AGCCCTCAG GCCCGGCCTA GTGCGGCCCA GTGCCTCTCC
1351 CACCCCTGGT TCCTGAAATC CATGCCTGCG GAGGAGGCCC ACTTCATCAA
1401 CACCAAGCAG CTCAGATTCC TCCTGGCCCG AAGTCGCTGG CAGCGTTCCC
1451 TGATGAGCTA CAAGTCCATC CTGGTGATGC GCTCCATCCC TGAGCTGCTG
1501 CGGGGCCAC CCAGACAGCC CTCCCTCGGC GTAGCCCGGC ACCTCTGCAG
1551 GGACACTGGT GGCTCCTCCA GTTCTCTCTC CTCCTCTGAC AACGAGCTCG
1601 CCCCATTTGC CCGGGCTAAG TCACTGCCAC CCTCCCGGTG GACACACTCA
1651 CCACTGTGTC ACCCCCGGGG CTTCCTGCGG CCCTCGGCCA GCCTGCCTGA
1701 GGAAGCCGAG GCCAGTGAGC GCTCCACCGA GGCCCCAGCT CCGCTGCAT
1751 CTCCCAGGGG TGCCGGGCCA CCGGCCGCCC AGGGCTGCGT GCCCGGCAC
1801 AGCGTCATCC GCAGCCTGTT CTACCACAG GCGGGTGAGA GCCCTGAGCA
1851 CGGGGCCCTG GCCCGGGGA GCAGGCGGCA CCCGGCCCGG CCGCGGCACC
1901 TGCTGAAGGG CGGTACATT GCGGGGCGCG TGCCAGGCCT GCGCGAGCCA
1951 CTGATGAGAG ACCGCGTGCT GGAGGAGGAG GCCGCCAGGG AGGAGCAGGC
2001 CACCCCTCTG GCCAAAGCCC CCTCATTGCA GACTGCCCTC CGGCTGCCTG
2051 CCTCTGGCAC CCACTTGGCC CTTGGCCACA GCCACTCCCT GGAACATGAC
2101 TCTCCGAGCA CCCCCCGCCC CTCTCGGAG GCCTGCGGTG AGGCACAGCG
2151 ACTGCCTTCA GCCCCTCCG GGGGGGCCCC TATCAGGGAC ATGGGGCACC
2201 CTCAGGGCTC CAAGCAGCTT CCATCCACTG GTGGCCACCC AGGCACTGCT
2251 CAGCCAGAGA GGCCATCCCC GGACAGCCCT TGGGGGCAGC CAGCCCTTTT
2301 CTGCCACCCC AAGCAGGGTT CTGCCCCCA GAGGGGCTGC AGCCCCCACC
2351 CAGCAGTTGC CCCATGCCCT CTTGGCTCCT TCCCTCCAGG ATCTTGCAAA
2401 GAGGCCCCCT TAGTACCCTC AAGCCCCCTC TTGGGACAGC CCCAGGCACC
2451 CCCTGCCCTT GCCAAAGCAA GCCCCCCATT GGAATCTAAG ATGGGGCCTG
2501 GAGACATCTC TCTTCTGGG AGGCCAAAAC CCGGCCCTG CAGTTCCCCA
2551 GGGTCAGCCT CCCAGGCGAG CTCTTCCCA GTGAGCTCCC TCAGGGTGGG
2601 CTCCTCCAG GTGGGCACAG AGCCTGGCCC CTCCCTGGAT GCGGAGGGCT
2651 GGACCCAGGA GGCTGAGGAT CTGTCCGACT CCACACCCAC CTGCAAGCGG
2701 CCTCAGGAAC AGGTGACCAT GCGCAAGTTC TCCCTGGGTG GTCGCGGGGG
2751 CTACGCAGGC GTGGCTGGCT ATGGCACCTT TGCCTTTGGT GGAGATGCAG
2801 GGGGCATGCT GGGGCAGGGG CCCATGTGGG CCAGGATAGC CTGGGCTGTG
2851 TCCCAGTCGG AGGAGGAGGA GCAGGAGGAG GCCAGGGCTG AGTCCCAGTC
2901 GGAGGAGCAG CAGGAGGCCA GGGCTGAGAG CCCACTGCCC CAGGTCAGTG
2951 CAAGGCCTGT GCCTGAGGTC GGCAGGGCTC CCACCAGGAG CTCTCCAGAG
3001 CCCACCCAT GGGAGGACAT CCGGCAGGTC TCCCTGGTGC AGATCCGGGA
3051 CCTGTGAGGT GATGCGGAGG CGGCCGACAC AATATCCCTG GACATTTCCG
3101 AGGTGAGACC CGCTACCTC AACCTCTCAG ACCTGTACGA TATCAAGTAC
3151 CTCCTATTCT AGTTTATGAT CTTAGGAAA GTCCCCAAGT CCGCTCAGCC
3201 AGAGCCGCCC TCCCCATGG CTGAGGAGGA GCTGGCCGAG TTCCCGGAGC
3251 CCACGTGGCC CTGGCCAGGT GAACTGGGCC CCCACGCAGG CCTGGAGATC
3301 ACAGAGGAGT CAGAGGATGT GGACGCGCTG CTGGCAGAGG CTGCCGTGGG
3351 CAGGAAGCGC AAGTGGTCCT CGCCGTACAG CAGCCTCTTC CACTTCCCTG
3401 GGAGGCACCT GCCGCTGGAT GAGCCTGCAG AGCTGGGGCT GCGTGAGAGA
3451 GTGAAGGCCT CCGTGAGCA CATCTCCCG ATCCTGAAGG GCAGGCCGGA
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FIGURE 3A

Docket No.: CL000927-CIP-DIV2

Serial No.: To b assigned

Inventors: Ming-Hui WEI et al.

Title: ISOLATED HUMAN KINASE PROTEINS...

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3501 AGGTCTGGAG AAGGAGGGGC CCCCAGGAA GAAGCCAGGC CTGCTTCCT
3551 TCCGGCTCTC AGGTCTGAAG AGCTGGGACC GAGCGCCGAC ATTCCTAAGG
3601 GAGCTCTCAG ATGAGACTGT GGTCTGGGC CAGTCAGTGA CACTGGCCTG
3651 CCAGGTGTCA GCCCAGCCAG CTGCCCAGGC CACCTGGAGC AAAGACGGAG
3701 CCCCCCTGGA GAGCAGCAGC CGTGTCTCA TCTCTGCCAC CCTCAAGAAC
3751 TTCCAGCTTC TGACCATCCT GGTGGTGGTG GCTGAGGACC TGGGTGTGTA
3801 CACCTGCAGC GTGAGCAATG CGCTGGGGAC AGTGACCACC ACGGGCGTCC
3851 TCCGGAAGGC AGAGCGCCCC TCATCTTCGC CATGCCCGGA TATCGGGGAG
3901 GTGTACGCGG ATGGGGTGCT GCTGGTCTGG AAGCCCGTGG AATCCTACGG
3951 CCCTGTGACC TACATTGTGC AGTGCAGCCT AGAAGGCGGC AGCTGGACCA
4001 CACTGGCCTC CGACATCTTT GACTGCTGCT ACCTGACCAG CAAGCTCTCC
4051 CGGGGTGGCA CCTACACCTT CCGCACGGCA TGTGTCAGCA AGGCAGGAAT
4101 GGTCTCCGCG AGCAGCCCCT CGGAGCAAGT CCTCTGGGA GGGCCAGCC
4151 ACCTGGCCTC TGAGGAGGAG AGCCAGGGGC GGTGAGCCCA ACCCTGCCCC
4201 AGCACAAGA CTTTCGCATT CCAGACACAG ATCCAGAGGG GCCGCTTCAG
4251 CGTGGTGC GGCAATGTGGG AGAAGGCCAG CGGGCGGGCG CTGGCCGCCA
4301 AGATCATCCC CTACCACCCC AAGGACAAGA CAGCAGTGCT GCGCGAATAC
4351 GAGGCCCTCA AGGGCCTGCG CCACCCGCAC CTGGCCAGC TGCACGCAGC
4401 CTACCTCAGC CCCCAGCACC TGGTGTCTAT CTTGGAGCTG TGCTCTGGGC
4451 CCAGAGTGCT CCCCTGCCTG GCCGAGAGGG CCTCCTACTC AGAATCTGAG
4501 GTGAAGGACT ACCTGTGGCA GATGTTGAGT GCCACCCAGT ACCTGCACAA
4551 CCAGCACATC CTGCACCTGG ACCTGAGGTC CGAGAACATG ATCATACCG
4601 AATACAACCT GCTCAAGGTC GTGGACCTGG GCAATGCACA GAGCCTCAGC
4651 CAGGAGAAGG TGCTGCCCTC AGACAAGTTC AAGGACTACC TAGAGACCAT
4701 GGCTCCAGAG CTCCTGGAGG GCCAGGGGGC TGTTCCACAG ACAGACATCT
4751 GGGCCATCGG TGTGACAGCC TTCATCATGC TGAGCGCCGA GTACCCGGTG
4801 AGCAGCGAGG GTGCACGCGA CCTGCAGAGA GGAATGCGCA AGGGGCTGGT
4851 CCGGCTGAGC CGCTGTACG CGGGGCTGTC CGGGGGCGCC GTGGCCTTCC
4901 TGCGCAGCAC TCTGTGCGCC CAGCCCTGGG GCCGGCCCTG CGCGTCCAGC
4951 TGCTGTCAGT GCCCGTGGCT AACAGAGGAG GGCCCGGCCT GTTCGCGGCC
5001 CGCGCCCGTG ACCTTCCCTA CCGCGCGGCT GCGCGTCTTC GTGCGCAATC
5051 GCGAGAAGAG ACGCGCGCTG CTGTACAAGA GGCACAACCT GGCCAGGTG
5101 CGCTGAGGGT CGCCCCGGCC ACACCCTTGG TCTCCCCGCT GGGGGTCGCT
5151 GCAGACGCGC CAATAAAAC GCACAGCCGG GCGAGAAAAA AAAAAAAAAA
5201 AAAAAA (SEQ ID NO:3)
```

FEATURES:

Start: 109
Exon: 109-5103
Stop: 5104

SNPs:

DNA				Protein		
Position	Major	Minor	Domain	Position	Major	Minor
311	T	C G	Exon	68	V	A G
1741	C	T	Exon	545	P	S
2714	T	C	Exon	869	V	A
2745	C	T	Exon	879	R	R
2859	A	G	Exon	917	S	S
3420	T	C	Exon	1104	D	D

Context:

DNA
Position

```
311 AACTCCTTCTGATCACCTGGCCAGCTGAGGTCAGAGTGGGAGAGGCAGTGGTTCATTGA
AGGAGTACTCCTAACTGTCAGAAGCCTGGGCGGTGAGGATGGGGTGCTGTCGCTTGGGCT
GCGGGGGGTGTTTCAGTTGCCACAGTGTATCTCAGGGTCTCACCAACCATCCAAGCATGG
TAGGCTGTGGCTGGCACCCAGGGTTGTGTGGCTGGGAGGTGGTCTCCACAGTTCCTTCC
CTGCCCTCCAGGGCCCCCATCCATGCAGGTAACCATCGAGGATGTGCAGGCACAGACAG
[T, C, G]
CGGAACGGCCCCAATTCGAGGCTATCATGAGGGCGACCCACAGCCCTCGGTGACCTGGTA
CAAGGACAGCGTCCAGCTGGTGGACAGCACCCGGCTTAGCCAGCAGCAAGAAGGCACCAC
ATACTCCCTGGTGTGAGGCATGTGGCTCGAAGGATGCCGGCGTTTACACCTGCCTGGC
CCAAAACACTGGTGGCCAGGTGCTCTGCAAGGCAGAGCTGCTGGTGTGGGGGGGACAA
TGAGCCGGACTCAGAGAAGCAAAGCCACCGGAGGAAGCTGCACTCCTTCTATGAGGTCAA
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FIGURE 3B

Docket No.: CL000927-CIP-DIV2
Serial No.: To be assigned
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN KINASE PROTEINS...

1741 CAGCGTTCCCTGATGAGCTACAAGTCCATCCTGGTGATGCGCTCCATCCCTGAGCTGCTG
GGGGGCCACCCGACAGCCCTCCCTCGGCGTAGCCCGGCACCTCTGCAGGGACACTGGT
GGCTCCTCAGTTCTCCTCCTCTGACAACGAGCTCGCCCCATTGCCCCGGGCTAAG
TCACTGCCACCCTCCCCGGTGACACACTCACCCTGCTGCACCCCCGGGGCTTCTGCGG
CCCTCGGCGAGCTGCCTGAGGAAGCCGAGGCCAGTGAGCGCTCCACCGAGGCCAGCT
[C, T]
CGCCTGCATCTCCCGAGGGTGCCGGGCCACCGGCCGCCAGGGCTGCGTGCCCCGGCACA
GCGTCATCCGAGCCTGTTCTACCACAGGCGGGTGAGAGCCCTGAGCACGGGGCCCTGG
CCCCGGGAGCAGGCGGCACCCGGCCCGCGCGGCACCTGCTGAAGGGCGGTACATG
CGGGGCGCTGCCAGGCTGCGCGAGCCACTGATGGAGCACCGCGTGCTGGAGGAGGAGG
CCGCGAGGAGGAGCAGGCCACCTCCTGGCCAAAGCCCCCTATTGAGACTGCCCTCC

2714 TACCCTCAAGCCCTTCTTGGGACAGCCCCAGGCACCCCTGCCCTGCCAAAGCAAGCC
CCCCATTGAGCTCTAAGATGGGGCCTGGAGACATCTCTTCTTGGGAGGCCAAAACCCG
GCCCTTGAGTTCCCCAGGGTCAGCCTCCAGGCGAGCTCTTCCCAAGTGAGCTCCCTCA
GGGTGGGCTCCTCCAGGTGGGCACAGAGCCTGGCCCCCTCCCTGGATGCGGAGGGCTGGA
CCAGGAGGCTGAGGATCTGTCCGACTCCACACCCACCTTGACGCGGCTCAGGAACAGG
[T, C]
GACCATGCGCAAGTTCTCCCTGGGTGGTGCGGGGGCTACGCAGGCGTGGCTGGCTATGG
CACCTTTGCCCTTGGTGGAGATGCAGGGGGCATGCTGGGGCAGGGGCCATGTGGGCCAG
GATAGCCTGGGGCTGTGTCCAGTCCGAGGAGGAGGAGCAGGAGGAGGCCAGGGCTGAGTC
CCAGTCGGAGGAGCAGCAGGAGGCCAGGGCTGAGAGCCCACTGCCCCAGGTGAGTCAAG
GCCTGTGCTGAGGTGCGCAGGGCTCCACAGGAGCTCTCCAGAGCCACCCATGGGA

2745 GGCACCCCTGCCCTGCCAAAGCAAGCCCCCATTGGACTCTAAGATGGGGCCTGGAGA
CATCTCTCTTCTGGGAGGCCAAAACCCGGCCCTGCAGTTCCCCAGGGTCAGCCTCCCA
GGCGAGCTCTTCCCAAGTGAGCTCCCTCAGGGTGGGCTCCTCCAGGTGGGCACAGAGCC
TGGCCCCCTCCCTGGATGCGGAGGGCTGGACCCAGGAGGCTGAGGATCTGTCCGACTCCAC
ACCCACCTTGACGCGCCTCAGGAACAGGTGACCATGCGCAAGTTCTCCCTGGGTGGTGC
[C, T]
GGGGGCTACGCAGGCGTGGCTGGCTATGGCACCTTTGCCTTTGGTGGAGATGCAGGGGC
ATGCTGGGGCAGGGGCCATGTGGGCCAGGATAGCCTGGGCTGTGTCCAGTCGGAGGAG
GAGGAGCAGGAGGAGGCCAGGGCTGAGTCCAGTCCGAGGAGCAGCAGGAGGCCAGGGCT
GAGAGCCCACTGCCCCAGGTGAGTCAAGGCCTGTGCCTGAGGTGCGCAGGGCTCCACC
AGGAGCTCTCCAGAGCCACCCATGGGAGGACATCGGGCAGGTCTCCCTGGTGCAATC

2859 CTCCCAGGCGAGCTCTTCCCAAGTGAGCTCCCTCAGGGTGGGCTCCTCCAGGTGGGCAC
AGAGCCTGGCCCTCCTGGATGCGGAGGGCTGGACCCAGGAGGCTGAGGATCTGTCCGA
TCCACACCCACCTTGAGCGGCTCAGGAACAGGTGACCATGCGCAAGTTCTCCCTGGG
TGCTGCGGGGGCTACGCAGGCGTGGCTGGCTATGGCACCTTTGCCTTTGGTGGAGATGC
AGGGGGCATGTGGGGCAGGGGCCATGTGGGCCAGGATAGCCTGGGCTGTGTCCAGTC
[A, G]
GAGGAGGAGGAGCAGGAGGAGGCCAGGGCTGAGTCCAGTCCGAGGAGCAGCAGGAGGCC
AGGGCTGAGAGCCCACTGCCCCAGGTGAGTCAAGGCCTGTGCCTGAGGTGCGCAGGGCT
CCCACCAGGAGCTCTCCAGAGCCACCCATGGGAGGACATCGGGCAGGTCTCCCTGGTG
CAGATCCGGGACCTGTGAGGTGATGCGGAGGCGGCCGACACAATATCCCTGGACATTTCC
GAGGTGGACCCCGCTACCTCAACCTCTCAGACCTGTACGATATCAAGTACCTCCATTTC

3420 CAACCTCTCAGACCTGTACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAA
AGTCCCCAAGTCCGCTCAGCCAGAGCCGCTCCCCATGGCTGAGGAGGAGCTGGCCGA
GTTCCCGAGCCACGTGGCCCTGGCCAGGTGAAGTGGGCCCCACGCAGGCTGGAGAT
CACAGAGGAGTCAGAGGATGTGGACGCGCTGCTGGCAGAGGCTGCCGTGGGCAGGAAGCG
CAAGTGGTCTCGCGTCACGCAGCTCTTCCACTTCCCTGGGAGGCACCTGCCGCTGGA
[T, C]
GAGCCTGCAGAGCTGGGGCTGCGTGAGAGAGTGAAGGCCTCCGTGGAGCACATCTCCCG
ATCCTGAAGGGCAGGCGGAAGGTCTGGAGAAGGAGGGGCCCCAGGAAGAAGCCAGGC
CTTGCTTCTTCCGGCTCTCAGGTCTGAAGAGCTGGGACCGAGCGCCGACATTCCTAAGG
GAGCTCTCAGATGAGACTGTGGTCTCTGGGCCAGTCACTGACACTGGCCTGCCAGGTGTCA
GCCAGCCAGCTGCCAGGCCACCTGGAGCAAAGACGAGGCCCCCTGGAGAGCAGCAGC

Chromosome map position: 1

Bac accession number: AC023889

FIGURE 3C